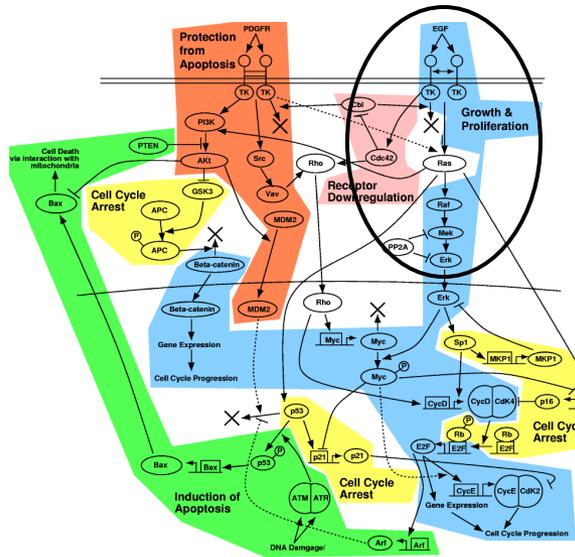


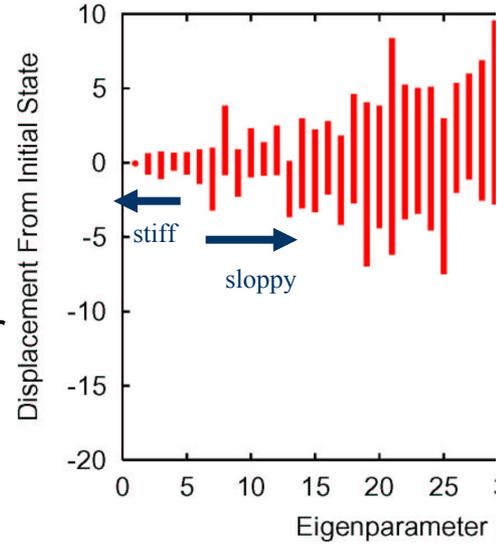
Stat Mech for Sloppy Models:

Protein Interactions in Cells

Sethna, Kevin Brown, Josh Waterfall, Fergal Casey, Ryan Gutenkuntz



- Proteins, RNA, DNA dynamics
- Monte Carlo in Model Space
- Renormalized Parameters
- Sloppy Modes
- Useful Predictions
- Understanding Cell Cycle, Cancer



Work in 48 dimensions
Gauge Invariance
“Symmetry”-breaking fields
“Replicas” ...

Cellular Regulatory Network

- Proliferation from EGF
- Differentiation from NGF
- 59 parameters, 68 data points
- 5 parameters can fit an elephant

